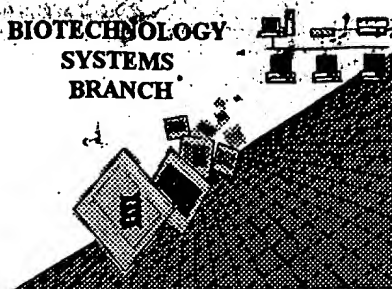


RAW SEQUENCE LISTING **ERROR REPORT**

BIOTECHNOLOGY
SYSTEMS
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number:

09/673,274

Source:

Per/09

Date Processed by STIC:

8/1/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 09/613,274
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE		
1 _____ Wrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 _____ Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 _____ Misaligned Amino Numbering	The numbering under each 5 th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.	
4 _____ Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5 _____ Variable Length	Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 _____ PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
7 _____ Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.	
8 _____ Skipped Sequences (NEW RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000	
9 _____ Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
10 _____ Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence	
11 _____ Use of <220>	Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)	
12 _____ PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 _____ Misuse of n	n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.	

PCT09

*delete extra
1107's - only*

RAW SEQUENCE LISTING

DATE: 08/01/2001

PATENT APPLICATION: US/09/673,274

TIME: 19:08:03

one 1107

should be shown

Input Set : A:\98015seq.txt

Output Set: N:\CRF3\08012001\I673274.raw

W--> 3 <110> APPLICANT: LAMBERTY, MIREILLE
W--> 4 ~~<110>~~ APPLICANT: BULET, PHILIPPE
W--> 5 ~~<110>~~ APPLICANT: BROOKHART, GARY
W--> 6 ~~<110>~~ APPLICANT: HOFFMAN, JULES
8 <120> TITLE OF INVENTION: GENE CODING FOR HELIOMICINE, AND USE THEREOF
10 <130> FILE REFERENCE: A33595 PCT USA
12 <140> CURRENT APPLICATION NUMBER: US 09/673,274
13 ~~<141>~~ CURRENT FILING DATE: 1999-07-12
15 <150> PRIOR APPLICATION NUMBER: PCT/FR99/00843
16 <151> PRIOR FILING DATE: 1999-04-12
18 <150> PRIOR APPLICATION NUMBER: FR 98 04933
19 <151> PRIOR FILING DATE: 1998-04-15
21 <160> NUMBER OF SEQ ID NOS: 38
23 <170> SOFTWARE: PatentIn Ver. 2.1

Does Not Comply
Corrected Diskette Needed

pg 1-8

ERRORED SEQUENCES

25 <210> SEQ ID NO: 1
26 <211> LENGTH: 147
E--> 27 <212> TYPE: ADN *DNA* *global errors*
28 <213> ORGANISM: synthetic construct *see item 10 on Error Summary Sheet*
30 <220> FEATURE:
31 <221> NAME/KEY: CDS
32 <222> LOCATION: (1)..(147)
34 <400> SEQUENCE: 1
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36 Ser Leu Asp Lys Arg Asp Lys Leu Ile Gly Ser Cys Val Trp Gly Ala
37 1 5 10 15
39 gtc aac tac act agt gac tgc aac ggc gag tgc aag cgc cgc ggt tac 96
40 Val Asn Tyr Thr Ser Asp Cys Asn Gly Glu Cys Lys Arg Arg Gly Tyr
41 20 25 30
43 aag ggt ggc cat tgt gga tcc ttc gct aac gtt aac tgt tgg tgt gaa 144
44 Lys Gly Gly His Cys Gly Ser Phe Ala Asn Val Asn Cys Trp Cys Glu
45 35 40 45
47 acc 147
48 Thr
51 <210> SEQ ID NO: 2
52 <211> LENGTH: 169
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54 <213> ORGANISM: synthetic construct
56 <220> FEATURE:
57 <221> NAME/KEY: CDS
58 <222> LOCATION: (1)..(132)
60 <400> SEQUENCE: 2
61 gat aag ctt atc ggt tcc tgc gtg tgg ggt gct gtg aac tac act tcc 48
62 Asp Lys Leu Ile Gly Ser Cys Val Trp Gly Ala Val Asn Tyr Thr Ser

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Input Set : A:\98015seq.txt

Output Set: N:\CRF3\08012001\I673274.raw

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63      1              5              10              15
65 gat tgc aac ggt gag tgc aag agg agg ggt tac aag ggt ggt cac tgc   96
66 Asp Cys Asn Gly Glu Cys Lys Arg Arg Gly Tyr Lys Gly Gly His Cys
67              20              25              30
69 ggt tcc ttc gct aac gtg aac tgc tgg tgc gag act tgagagctcg   142
70 Gly Ser Phe Ala Asn Val Asn Cys Trp Cys Glu Thr
71              35              40
73 gcgaggcgaa cgtgtcgacg gatccgg   169
76 <210> SEQ ID NO: 3
77 <211> LENGTH: 261
E--> 78 <212> TYPE: (ADN)
79 <213> ORGANISM: (synthetic construct)
81 <220> FEATURE:
82 <221> NAME/KEY: CDS
83 <222> LOCATION: (3)..(224)
85 <400> SEQUENCE: 3
86 cc atg ggt ttc gtg ctt ttc tct cag ctt cca tct ttc ctt ctt gtg   47
87   Met Gly Phe Val Leu Phe Ser Gln Leu Pro Ser Phe Leu Leu Val
88      1              5              10              15
90 tct act ctt ctt ctt ttc ctt gtg atc tct cac tct tgc cgt gcc gat   95
91 Ser Thr Leu Leu Leu Phe Leu Val Ile Ser His Ser Cys Arg Ala Asp
92              20              25              30
94 aag ctt atc ggt tcc tgc gtg tgg ggt gct gtg aac tac act tcc gat   143
95 Lys Leu Ile Gly Ser Cys Val Trp Gly Ala Val Asn Tyr Thr Ser Asp
96              35              40              45
98 tgc aac ggt gag tgc aag agg agg ggt tac aag ggt ggt cac tgc ggt   191
99 Cys Asn Gly Glu Cys Lys Arg Arg Gly Tyr Lys Gly Gly His Cys Gly
100              50              55              60
102 tcc ttc gct aac gtg aac tgc tgg tgc gag act tgagagctcg gcgaggcgaa 244
103 Ser Phe Ala Asn Val Asn Cys Trp Cys Glu Thr
104      65              70
106 cgtgtcgacg gatccgg   261
109 <210> SEQ ID NO: 4
110 <211> LENGTH: 120
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112 <213> ORGANISM: (synthetic construct)
114 <220> FEATURE:
115 <221> NAME/KEY: CDS
116 <222> LOCATION: (12)..(101)
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120   Met Gly Phe Val Leu Phe Ser Gln Leu Pro Ser Phe Leu
121      1              5              10
123 ctt gtg tct act ctt ctt ctt ttc ctt gtg atc tct cac tct tgc cgt   98
124 Leu Val Ser Thr Leu Leu Leu Phe Leu Val Ile Ser His Ser Cys Arg
125      15              20              25
127 gct ggagacgcga attcacaca   120
128 Ala
129 30

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RAW SEQUENCE LISTING

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Input Set : A:\98015seq.txt

Output Set: N:\CRF3\08012001\I673274.raw

280 <220> FEATURE:

281 <221> NAME/KEY: CDS

282 <222> LOCATION: (7)..(204)

284 <400> SEQUENCE: 18

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286      Met Ala Cys Thr Asn Asn Ala Met Arg Ala Leu Phe Leu Leu
287      1              5              10
289 ctg ctc ttc tgc atc gtg cac ggc gat aag ctt atc ggt tcc tgc gtg   96
290 Leu Leu Phe Cys Ile Val His Gly Asp Lys Leu Ile Gly Ser Cys Val
291 15              20              25              30
293 tgg ggt gct gtg aac tac act tcc gat tgc aac ggt gag tgc aag agg   144
294 Trp Gly Ala Val Asn Tyr Thr Ser Asp Cys Asn Gly Glu Cys Lys Arg
295      35              40              45
297 agg ggt tac aag ggt ggt cac tgc ggt tcc ttc gct aac gtg aac tgc   192
298 Arg Gly Tyr Lys Gly Gly His Cys Gly Ser Phe Ala Asn Val Asn Cys
299      50              55              60
301 tgg tgc gag act tgactcgag
302 Trp Cys Glu Thr
303      65
306 <210> SEQ ID NO: 19
307 <211> LENGTH: 838

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E--> 308 <212> TYPE: ADN

309 <213> ORGANISM: synthetic construct

311 <220> FEATURE:

312 <221> NAME/KEY: promoter

313 <222> LOCATION: (7)..(532)

315 <220> FEATURE:

316 <221> NAME/KEY: misc_structure

317 <222> LOCATION: (533)..(568)

319 <220> FEATURE:

320 <221> NAME/KEY: terminator

321 <222> LOCATION: (569)..(832)

323 <400> SEQUENCE: 19

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324 aagcttccag aaggtaatta tccaagatgt agcatcaaga atccaatggt tacgggaaaa 60
326 actatggaag tattatgtga gctcagcaag aagcagatca atatgcggca catatgcaac 120
328 ctatgttcaa aaatgaagaa tgtacagata caagatccta tactgccaga atacgaagaa 180
330 gaatacgtag aaattgaaaa agaagaacca ggcgaagaaa agaattcttga agacgtaagc 240
332 actgacgaca acaatgaaaa gaagaagata aggtcgggtga ttgtgaaaga gacatagagg 300
334 acacatgtaa ggtggaaaaat gtaagggcgg aaagtaacct tatcacaagg gaattattatc 360
336 cccactact tatcttttta tttttttccg tgtcattttt gcccttgagt tttctatat 420
338 aaggaaccaa gttcggcatt tgtgaaaaca agaaaaaatt tgggtgaagc tattttcttt 480
340 gaagtactga ggatacaact tcagagaaat ttgtaagttt gtagatctcg attctagaag 540
342 gcctgaattc gagctcggtg ccggatccaa ttcccgatcg ttcaaacatt tggcaataaa 600
344 gtttcttaag attgaatcct gttgccgggtc ttgcgatgat tatcatataa tttctgttga 660
346 attacgttaa gcatgtaata attaacatgt aatgcgatgac gttattttatg agatgggttt 720
348 ttatgattag agtcccgcga ttatacatgt aatacgcgat agaaaacaaa atatagcgcg 780
350 caaactagga taaattatcg cgcgcggtgt catctatggt actagatcgg ggatcgat 838

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353 <210> SEQ ID NO: 20

354 <211> LENGTH: 1036

RAW SEQUENCE LISTING

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Output Set: N:\CRF3\08012001\I673274.raw

132 <210> SEQ ID NO: 5
133 <211> LENGTH: 75
E--> 134 <212> TYPE: ADN
135 <213> ORGANISM: synthetic construct
137 <400> SEQUENCE: 5
138 gcgtcgacgc gatgggtttc gtgcttttct ctacgtttcc atottttcett cttgtgtcta 60
140 ctctttttct ttccc
143 <210> SEQ ID NO: 6 75
144 <211> LENGTH: 72
E--> 145 <212> TYPE: ADN
146 <213> ORGANISM: synthetic construct
148 <400> SEQUENCE: 6
149 tcgccggcac ggcaagagta agagatcaca aggaaaagaa gaagagtaga cacaagaagg 60
151 aaagatggaa gc
154 <210> SEQ ID NO: 7 72
155 <211> LENGTH: 80
E--> 156 <212> TYPE: ADN
157 <213> ORGANISM: synthetic construct
159 <400> SEQUENCE: 7
160 gataagetta tcggttcctg cgtgtgggggt gctgtgaact acacttcoga ttgcaacggg 60
162 gagtgcgaaga ggagggggtta
165 <210> SEQ ID NO: 8 80
166 <211> LENGTH: 109
E--> 167 <212> TYPE: ADN
168 <213> ORGANISM: synthetic construct
170 <400> SEQUENCE: 8
171 ccggatccgt cgacacgttc gcctcgccga gctctcaagt ctgcaccag cagttcacgt 60
173 tagcgaagga accgcagtga ccaccttgt aacctctcct cttgcactc 109
176 <210> SEQ ID NO: 9
177 <211> LENGTH: 85
E--> 178 <212> TYPE: ADN
179 <213> ORGANISM: synthetic construct
181 <400> SEQUENCE: 9
182 agggcccccct aggggtttaa cggccagtca ggccgaattc gagctcggtta cccgggggac 60
184 ctctagagtc gacctgcagg catgc
187 <210> SEQ ID NO: 10 85
188 <211> LENGTH: 66
E--> 189 <212> TYPE: ADN
190 <213> ORGANISM: synthetic construct
192 <400> SEQUENCE: 10
193 ccctgaacca ggctcgaggg cgcgccttaa taaaagctt gcatgcctgc aggtcgactc 60
195 tagagg
198 <210> SEQ ID NO: 11 66
199 <211> LENGTH: 93
E--> 200 <212> TYPE: ADN
201 <213> ORGANISM: synthetic construct
203 <400> SEQUENCE: 11
204 ccggccagtc aggccacact taattaagtt taaacgcggc cccggcgcg ctaggtgtgt 60
206 gctcgagggc ccaacctcag tacctggttc agg 93

RAW SEQUENCE LISTING

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Input Set : A:\98015seq.txt

Output Set: N:\CRF3\08012001\I673274.raw

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209 <210> SEQ ID NO: 12
210 <211> LENGTH: 93
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212 <213> ORGANISM: synthetic construct
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215 ccggcctgaa ccaggtactg aggttgggcc ctcgagcaca cacctaggcg cgccgggggcc 60
217 gcgtttaaac ttaattaagt gtggcctgac tgg 93
220 <210> SEQ ID NO: 13
221 <211> LENGTH: 50
E--> 222 <212> TYPE: ADN
223 <213> ORGANISM: synthetic construct
225 <400> SEQUENCE: 13
226 ggtctagaat ggcctgcacc aacaacgccca tgagggccct ctctctctc 50
229 <210> SEQ ID NO: 14
230 <211> LENGTH: 50
E--> 231 <212> TYPE: ADN
232 <213> ORGANISM: synthetic construct
234 <400> SEQUENCE: 14
235 ccgaattcgg cgccgtgcac gatgcagaag agcacgagga ggaagagggc 50
238 <210> SEQ ID NO: 15
239 <211> LENGTH: 81
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241 <213> ORGANISM: synthetic construct
243 <220> FEATURE:
244 <221> NAME/KEY: CDS
245 <222> LOCATION: (7)..(72)
247 <400> SEQUENCE: 15
248 tctaga atg gcc tgc acc aac aac gcc atg agg gcc ctc ttc ctc ctc 48
249 Met Ala Cys Thr Asn Asn Ala Met Arg Ala Leu Phe Leu Leu
250 1 5 10
252 ctg ctc ttc tgc atc gtg cac ggc gccgaattc 81
253 Leu Leu Phe Cys Ile Val His Gly
254 15 20
257 <210> SEQ ID NO: 16
258 <211> LENGTH: 24
E--> 259 <212> TYPE: ADN
260 <213> ORGANISM: synthetic construct
262 <400> SEQUENCE: 16
263 gataagctta tcggttcctg cgtg 24
266 <210> SEQ ID NO: 17
267 <211> LENGTH: 32
E--> 268 <212> TYPE: ADN
269 <213> ORGANISM: synthetic construct
271 <400> SEQUENCE: 17
272 ggctcgagtc aagtctcgca ccagcagttc ac 32
275 <210> SEQ ID NO: 18
276 <211> LENGTH: 213
E--> 277 <212> TYPE: ADN
278 <213> ORGANISM: synthetic construct

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RAW SEQUENCE LISTING

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TIME: 19:08:03

Input Set : A:\98015seq.txt

Output Set: N:\CRF3\08012001\I673274.raw

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E--> 355 <212> TYPE: ADN
356 <213> ORGANISM: synthetic construct
358 <220> FEATURE:
359 <221> NAME/KEY: promoter
360 <222> LOCATION: (7)..(532)
362 <220> FEATURE:
363 <221> NAME/KEY: CDS
364 <222> LOCATION: (539)..(736)
366 <220> FEATURE:
367 <221> NAME/KEY: terminator
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373 actatggaag tattatgtga gctcagcaag aagcagatca atatgcgga catatgcaac 120
375 ctatgttcaa aaatgaagaa tgtacagata caagatccta tactgccaga atacgaagaa 180
377 gaatacgtag aaattgaaaa agaagaacca ggcgaagaaa agaattctga agacgtaagc 240
379 actgacgaca acaatgaaaa gaagaagata aggtcgggtga ttgtgaaaga gacatagagg 300
381 acacatgtaa ggtggaaaat gtaagggcgg aaagtaacct tatcacaag gaatcttacc 360
383 cccactact taccctttta tttttttccg tgtcattttt gcccttgagt tttcctatat 420
385 aaggaaccaa gttcggcatt tgtgaaaaca agaaaaaatt tgggtgtaagc tttttctttt 480
387 gaagtactga ggatacaact tcagagaaat ttgtaagttt gtagatctcg attctaga 538
389 atg gcc tgc acc aac aac gcc atg agg gcc ctc ttc ctc ctc gtg ctc 586
390 Met Ala Cys Thr Asn Asn Ala Met Arg Ala Leu Phe Leu Leu Val Leu
391 1 5 10 15
393 ttc tgc atc gtg cac ggc gat aag ctt atc ggt tcc tgc gtg tgg ggt 634
394 Phe Cys Ile Val His Gly Asp Lys Leu Ile Gly Ser Cys Val Trp Gly
395 20 25 30
397 gct gtg aac tac act tcc gat tgc aac ggt gag tgc aag agg agg ggt 682
398 Ala Val Asn Tyr Thr Ser Asp Cys Asn Gly Glu Cys Lys Arg Arg Gly
399 35 40 45
401 tac aag ggt ggt cac tgc ggt tcc ttc gct aac gtg aac tgc tgg tgc 730
402 Tyr Lys Gly Gly His Cys Gly Ser Phe Ala Asn Val Asn Cys Trp Cys
403 50 55 60
405 gag act tgactcgagg gggggcccggt taccggatcc aattcccgat cgttcaaaca 786
406 Glu Thr
407 65
409 tttggcaata aagtttctta agattgaatc ctgttgccgg tcttgcgatg attatcatat 846
411 aattttctgtt gaattacgtt aagcatgtaa taattaacat gtaatgcatg acgttattta 906
413 tgagatgggt ttttatgatt agagtccgcg aattatacat ttaatacgcg atagaaaaca 966
415 aaatatagcg cgcaaactag gataaattat cgcgcgcggt gtcattctatg ttactagatc 1026
417 ggggatcgat 1036
420 <210> SEQ ID NO: 21
421 <211> LENGTH: 52
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423 <213> ORGANISM: synthetic construct
425 <400> SEQUENCE: 21
426 agcttgata aaagagacaa gttgattggc agctgtgttt ggggcgcggt ca 52
429 <210> SEQ ID NO: 22
430 <211> LENGTH: 56

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RAW SEQUENCE LISTING

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Input Set : A:\98015seq.txt

Output Set: N:\CRF3\08012001\I673274.raw

E--> 431 <212> TYPE: ADN
432 <213> ORGANISM: synthetic construct
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435 agtgtagttg acggcgcccc aaacacagct gccaatcaac ttgtctcttt tatcca 56
438 <210> SEQ ID NO: 23
439 <211> LENGTH: 52

E--> 440 <212> TYPE: ADN
441 <213> ORGANISM: synthetic construct
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447 <210> SEQ ID NO: 24
448 <211> LENGTH: 52

E--> 449 <212> TYPE: ADN
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456 <210> SEQ ID NO: 25
457 <211> LENGTH: 56

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459 <213> ORGANISM: synthetic construct
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465 <210> SEQ ID NO: 26
466 <211> LENGTH: 52

E--> 467 <212> TYPE: ADN
468 <213> ORGANISM: synthetic construct
470 <400> SEQUENCE: 26
471 gatctgtcga cctatcaggt ttcacaccaa cagttaacgt tagcgaagga tc 52
474 <210> SEQ ID NO: 27
475 <211> LENGTH: 42

E--> 476 <212> TYPE: ADN
477 <213> ORGANISM: synthetic construct
479 <400> SEQUENCE: 27
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483 <210> SEQ ID NO: 28
484 <211> LENGTH: 42

E--> 485 <212> TYPE: ADN
486 <213> ORGANISM: synthetic construct
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489 tcgacctatc aggttctaca ccaacagtta acgttagcga ag 42
492 <210> SEQ ID NO: 29
493 <211> LENGTH: 32

E--> 494 <212> TYPE: ADN
495 <213> ORGANISM: synthetic construct
497 <400> SEQUENCE: 29
498 ctagtgactg caacggcgag tgcttgttgc gc 32
501 <210> SEQ ID NO: 30
502 <211> LENGTH: 26

E--> 503 <212> TYPE: ADN

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/673,274

DATE: 08/01/2001

TIME: 19:08:03

Input Set : A:\98015seq.txt

Output Set: N:\CRF3\08012001\I673274.raw

```

504 <213> ORGANISM: synthetic construct
506 <400> SEQUENCE: 30
507 gcaacaagca ctcgccgttg cagtca 26
510 <210> SEQ ID NO: 31
511 <211> LENGTH: 32
E--> 512 <212> TYPE: ADN
513 <213> ORGANISM: synthetic construct
515 <400> SEQUENCE: 31
516 ctagtgactg cgctgctgag tgcaagcggc gc 32
519 <210> SEQ ID NO: 32
520 <211> LENGTH: 26
E--> 521 <212> TYPE: ADN
522 <213> ORGANISM: synthetic construct
524 <400> SEQUENCE: 32
525 gccgcttgca ctcagcagcg cagtca 26
528 <210> SEQ ID NO: 33
529 <211> LENGTH: 40
E--> 530 <212> TYPE: ADN
531 <213> ORGANISM: synthetic construct
533 <400> SEQUENCE: 33
534 agcttgata aaagagctgc tgctgctggt agctgtgttt 40
537 <210> SEQ ID NO: 34
538 <211> LENGTH: 18
E--> 539 <212> TYPE: ADN
540 <213> ORGANISM: synthetic construct
542 <400> SEQUENCE: 34
543 ggggcgccgt caactaca 18
546 <210> SEQ ID NO: 35
547 <211> LENGTH: 22
E--> 548 <212> TYPE: ADN
549 <213> ORGANISM: synthetic construct
551 <400> SEQUENCE: 35
552 ctagtgtagt tgacggcgcc cc 22
555 <210> SEQ ID NO: 36
556 <211> LENGTH: 36
E--> 557 <212> TYPE: ADN
558 <213> ORGANISM: synthetic construct
560 <400> SEQUENCE: 36
561 aaacacagct accagcagca gcagctcttt tatcca 36
564 <210> SEQ ID NO: 37
565 <211> LENGTH: 32
E--> 566 <212> TYPE: ADN
567 <213> ORGANISM: synthetic construct
569 <400> SEQUENCE: 37
570 ctagtgactg cgctgctgag tgcttggtgc gc 32
573 <210> SEQ ID NO: 38
574 <211> LENGTH: 26
E--> 575 <212> TYPE: ADN
576 <213> ORGANISM: synthetic construct

```

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/673,274

DATE: 08/01/2001

TIME: 19:08:03

Input Set : A:\98015seq.txt

Output Set: N:\CRF3\08012001\I673274.raw

578 <400> SEQUENCE: 38

579 gcaacaagca ctcagcagcg cagtca

26

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/673,274

DATE: 08/01/2001

TIME: 19:08:04

Input Set : A:\98015seq.txt

Output Set: N:\CRF3\08012001\I673274.raw

L:4 M:280 W: Numeric Identifier already exists, <110> found multiple times
L:5 M:280 W: Numeric Identifier already exists, <110> found multiple times
L:6 M:280 W: Numeric Identifier already exists, <110> found multiple times
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:27 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:53 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:78 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:111 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:134 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:145 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:156 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:167 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:178 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:189 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:200 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:211 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:222 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:231 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:240 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:259 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:268 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:277 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:308 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:355 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:422 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:431 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:440 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:449 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:458 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:467 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:476 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:485 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:494 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:503 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:512 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:521 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:530 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:539 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:548 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:557 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:566 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:575 M:310 E: (3) Wrong or Missing Sequence Type, TYPE: